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RAW SEQUENCE LISTING      DATE: 11/13/2000  
 PATENT APPLICATION: US/09/698,579      TIME: 15:58:16

Input Set : A:\Uvm-0001.app  
 Output Set: N:\CRF3\11132000\I698579.raw

**ENTERED**

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3 <110> APPLICANT: Bramley, John A.
4   Plaut, Karen I.
5   Kerr, David
7 <120> TITLE OF INVENTION: TREATMENT OF STAPHYLOCOCCUS INFECTIONS
9 <130> FILE REFERENCE: Mastitis
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/698,579
12 <141> CURRENT FILING DATE: 2000-10-27
14 <160> NUMBER OF SEQ ID NOS: 10
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1486
20 <212> TYPE: DNA
21 <213> ORGANISM: Staphylococcus simulans
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26 gtgtgtttgt atatttcac aaatcaaatc aatattattt tactttcttc atcggtaaaa 180
27 aatgtaatat ttataaaaa atgctattct cataaatgta ataataaatt aggaggtatt 240
28 aagggtgaag aaaacaaaa acaattatta tacgagacct ttagctattg gactgagtac 300
29 atttgcttta gcatctattg tttatggagg gattcaaaat gaaacacatg cttctgaaaa 360
30 aagtaaatat gatgtttcaa aaaaagtagc tgaagtagag acttcaaaag cccagtaga 420
31 aaatacagct gaagtagaga cttcaaaagc tccagtagaa aatacagctg aagtagagac 480
32 ttcaaaagct ccagtagaaa atacagctga agtagagact tcaaaagctc cagtagaaaa 540
33 tacagctgaa gttagagact caaaaagctc ggtagaaaat acagctgaag tagagacttc 600
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35 aacagcttta agagctgcaa cacatgaaca ttacagcaca tgggtgaata attacaaaaa 720
36 aggatatggt tacggctcct atccattagg tataaatggc ggtatgcact acggagttga 780
37 tttttttatg aatatttgaa caccagtaaa agctatttca agcggaaaaa tagttgaagc 840
38 tggttggagt aattacggag gaggtaatca aataggctct attgaaaatg atggagtgca 900
39 tagacaatyg tatatgcac taagtaataa gttaggagatt gtaggagatt atgtcaaaagc 960
40 tggtaaaata atcggttggc ctggaagcac tggttattct acagcaccac atttacactt 1020
41 ccaaagaatg gttaattcat ttcaaaattc aactgcccac gatccaatgc ctttcttaaa 1080
42 gagcycagga tatggaaaag caggtggtac agtaactcca acgccaataa caggttgga 1140
43 aacaaacaaa tatggcacac tataataaac agagtcagct agcttcacac ctaatacaga 1200
44 tataataaca agaacgactg gtccatttag aagcatgccg cagtcaggag tcttaaaagc 1260
45 aggtcaaaac attcattatg atgaagtgat gaaacaagac ggtcatgttt gggtaggtta 1320
46 tacaggtaac agtggccaac gtatttactt gcctgttaaga acatggaata aatctactaa 1380
47 tacttttagt gttctttggg gaactataaa gtgagcgcgc tttttataaa cttatatgat 1440
48 aattagagca aataaaaatt tttctcatt cctaaagttg aagctt 1486
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 388
53 <212> TYPE: PRT
54 <213> ORGANISM: Staphylococcus simulans
56 <400> SEQUENCE: 2
57 Met Lys Lys Thr Lys Asn Asn Tyr Tyr Thr Arg Pro Leu Ala Ile Gly
58 1 5 10 15
60 Leu Ser Thr Phe Ala Leu Ala Ser Ile Val Tyr Gly Gly Ile Gln Asn

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61          20          25          30
63 Glu Thr His Ala Ser Glu Lys Ser Asn Met Asp Val Ser Lys Lys Val
64          35          40          45
66 Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val
67          50          55          60
69 Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser
70 65          70          75          80
72 Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro
73          85          90          95
75 Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn
76          100         105         110
78 Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu
79          115         120         125
81 Val Glu Thr Ser Lys Ala Leu Val Gln Asn Arg Thr Ala Leu Arg Ala
82          130         135         140
84 Ala Thr His Glu His Ser Gln Trp Leu Asn Asn Tyr Lys Lys Gly Tyr
85 145         150         155         160
87 Gly Tyr Gly Pro Tyr Pro Leu Gly Ile Asn Gly Gly Met His Tyr Gly
88          165         170         175
90 Val Asp Glu Phe Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser
91          180         185         190
93 Gly Lys Ile Val Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln
94          195         200         205
96 Ile Gly Leu Ile Glu Asn Asp Gly Val His Arg Gln Glu Tyr Met His
97          210         215         220
99 Leu Ser Lys Tyr Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln
100 225         230         235         240
102 Ile Ile Gly Trp Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu
103          245         250         255
105 His Phe Gln Arg Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp
106          260         265         270
108 Pro Met Pro Phe Leu Lys Ala Ser Gly Tyr Gly Lys Ala Gly Gly Thr
109          275         280         285
111 Val Thr Pro Thr Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr
112          290         295         300
114 Leu Tyr Lys Ser Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile
115 305         310         315         320
117 Thr Arg Thr Thr Gly Pro Phe Arg Ser Met Pro Gln Ser Gly Val Leu
118          325         330         335
120 Lys Ala Gly Gln Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly
121          340         345         350
123 His Val Trp Val Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu
124          355         360         365
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127          370         375         380
129 Gly Thr Ile Lys
130 385
133 <210> SEQ ID NO: 3
134 <211> LENGTH: 741

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135 <212> TYPE: DNA
136 <213> ORGANISM: Staphylococcus simulans
138 <400> SEQUENCE: 3
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140 ggcccttatac cattaggtat aaatggcggg atgcactacg gagttgattt ttttatgaat 120
141 attggaacac cagtaaaagc tatttcaagc ggaaaaatag ttgaagctgg ttggagtaat 180
142 tacggaggag gtaaatcaaat aggtcttatt gaaaatgatg qagtgcatag acaatgggat 240
143 atgcatctaa gttaatatata tgttaagta ggagattatg tcaaaagctgg tcaataaatc 300
144 ggttggtctg gaagcactgg ttattctaca gcaccacatt tacacttcca aagaatgggt 360
145 aactcatttt cacagtcacac tgcccaagat ccaatgcctt tcttaagagag cgcagatat 420
146 ggaaaagcag gtggtacagt aactccaacg ccgaatacag gttggaaaac aaacaaatat 480
147 ggcacactat ataaatcaga gtcagctagc ttcacaccta atacagatat aataacaaga 540
148 acgactggtc catttagaag catgccgcag tcaggagtct taaaagcagg tcaaacatt 600
149 cattatgatg aagtgatgaa acaagacggg catgtttggg taggttatatc aggtaacagt 660
150 ggccaacgta tttacttgcc tgtgagaaca tggcagaagt ctactaatat tctgggtgtt 720
151 ctgtggggaa ctataaagt a
152
154 <210> SEQ ID NO: 4
155 <211> LENGTH: 1520
156 <212> TYPE: DNA
157 <213> ORGANISM: Staphylococcus simulans
159 <400> SEQUENCE: 4
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161 tcgcgcacccg tgtgaaccgc attgaggaat ggccgttcgg caagcgcctg tacggcctcg 120
162 atttgaacgt gcgtcgcaag acagcgtcgc gcccgcggtc agagtcgggc gcccgcggtg 180
163 tacggacagc gacgcggcg tccgccgatg acgaacggtc gtgcgcgtca gtcgcattgc 240
164 ccgctcgccg ctggcggttc ggcttcgcgg gcgcagcgcg gtccaccact cttcaaacgt 300
165 ctttctcggg agcagcatat gaagaagatt tccaagcgcg gactggggct ggcgctgggt 360
166 tgcgcgctgg cgacgatcgg cggcaacgca gcgcgcaggg ccacggctca gcggcgagga 420
167 tctggtgtat tctacgacga gatgttcgac ttcgacatcg atgcgcattt ggccaagcat 480
168 gcgcgcctac tgcacaagca ctgcggaagag atctcgcaact ggcccggtca cagcgggatc 540
169 agccgaagtg ttgatcgcgc tgatggagca gcagagcgcg cggtcacgcc aagcgcgcga 600
170 cgaatcgctc gttcgycagg ctggcgcgcg ccgacggctt cggcgcgcg ccccgcgagg 660
171 tcgcgctggc gctgcgcgag tcgctgtacg agcgcgatcc cgacgcgcc aagggcggt 720
172 gacgctggcc cgcgcgaatc cgtgcaggc gctgttcgag cgttcggcg acaacgagcc 780
173 ggcggcgcg ctgcgcggcg acggcgagtt ccagctggtc tacggcgcc tgttcaacga 840
174 accgcgcag gccaaaggcg cttcgacgc cttcgccaag gccggcccg acgtgcagcc 900
175 gtgtcgccca acggcctgct gcagttcccc ttcccgcgcg gcgccagctg gcatgtcgcc 960
176 ggcgccca ccaacaccgg ctgcggcaat taccgatgt cytcgctgga catgtcgcc 1020
177 ggcggcggt ggggcagcaa ccagaacggc aactgggtgt cggcctcgcc cgcggctcg 1080
178 ttcaagcgcc actcttcgtg cttcgcgag atcgtgcaca ccggcggtg gtcgacgacc 1140
179 tactaccacc tgatgaacat ccagtacaac accggcgcca acgtgtcgat gaacaccgcc 1200
180 atcgccaacc cggccaacac ccaggcgag gcgctytcga acggcgcca gtcgaccggc 1260
181 ccgcaagcgc attggtcggt gaagcagaac ggcagcttct accacctcaa cggcacctac 1320
182 ctgtcgggct atcgcatcac cgcgaccggc agcagctatg acaccaactg cagccgggtc 1380
183 tatctgacca agaacggcca gaaactactg tacggtatt acgtcaaccc ggcccgaaac 1440
184 tgaggctcgc cgcgtcggtt gccgcgctcc tcaagcgccc cagcgcgggg gcgcgggac 1500
185 cggccgggtc aggtcgaatt
186
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 480

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190 <212> TYPE: PRT
191 <213> ORGANISM: Staphylococcus simulans
193 <400> SEQUENCE: 5
194 Met Lys Lys Thr Lys Asn Asn Tyr Tyr Thr Thr Pro Leu Ala Ile Gly
195 1 5 10 15
197 Leu Ser Thr Phe Ala Leu Ala Ser Ile Val Tyr Gly Gly Ile Gln Asn
198 20 25 30
200 Glu Thr His Ala Ser Glu Lys Ser Asn Met Asp Val Ser Lys Lys Val
201 35 40 45
203 Ala Glu Val Glu Thr Ser Lys Pro Pro Val Glu Asn Thr Ala Glu Val
204 50 55 60
206 Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser
207 65 70 75 80
209 Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro
210 85 90 95
212 Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn
213 100 105 110
215 Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu
216 115 120 125
218 Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr
219 130 135 140
221 Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala
222 145 150 155 160
224 Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu
225 165 170 175
227 Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala
228 180 185 190
230 Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu
231 195 200 205
233 Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys
234 210 215 220
236 Ala Leu Val Gln Asn Arg Thr Ala Leu Arg Ala Ala Thr His Glu His
237 225 230 235 240
239 Ser Ala Gln Trp Leu Asn Asn Tyr Lys Tyr Gly Tyr Gly Tyr Gly Pro
240 245 250 255
242 Tyr Pro Leu Gly Ile Asn Gly Gly Ile His Tyr Gly Val Asp Phe Phe
243 260 265 270
245 Met Asn Ile Gly Thr Pro Val Lys Ala Ile Ser Ser Gly Lys Ile Val
246 275 280 285
248 Glu Ala Gly Trp Ser Asn Tyr Gly Gly Gly Asn Gln Ile Gly Leu Ile
249 290 295 300
251 Glu Asn Asp Gly Val His Arg Gln Trp Tyr Met His Leu Ser Lys Tyr
252 305 310 315 320
254 Asn Val Lys Val Gly Asp Tyr Val Lys Ala Gly Gln Ile Ile Gly Trp
255 325 330 335
257 Ser Gly Ser Thr Gly Tyr Ser Thr Ala Pro His Leu His Phe Gln Arg
258 340 345 350
260 Met Val Asn Ser Phe Ser Asn Ser Thr Ala Gln Asp Pro Met Pro Phe
261 355 360 365

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263 Leu Lys Ser Ala Gly Tyr Gly Lys Ala Gly Gly Thr Val Thr Pro Thr
264      370      375      380
266 Pro Asn Thr Gly Trp Lys Thr Asn Lys Tyr Gly Thr Leu Tyr Lys Ser
267 385      390      395      400
269 Glu Ser Ala Ser Phe Thr Pro Asn Thr Asp Ile Ile Thr Arg Thr Thr
270      405      410      415
272 Gly Pro Phe Arg Ser Met Pro Glu Ser Gly Val Leu Lys Ala Gly Gln
273      420      425      430
275 Thr Ile His Tyr Asp Glu Val Met Lys Gln Asp Gly His Val Trp Val
276      435      440      445
278 Gly Tyr Thr Gly Asn Ser Gly Gln Arg Ile Tyr Leu Pro Val Arg Thr
279      450      455      460
281 Trp Asn Lys Ser Thr Asn Thr Leu Gly Val Leu Trp Gly Thr Ile Lys
282 465      470      475      480
288 <210> SEQ ID NO: 6
289 <211> LENGTH: 492
290 <212> TYPE: PRT
291 <213> ORGANISM: Achromobacter lyticus
293 <400> SEQUENCE: 6
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298      20      25      30
300 Glu Thr His Ala Ser Glu Lys Ser Asn Met Asp Val Ser Lys Lys Val
301      35      40      45
303 Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val
304      50      55      60
306 Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser
307 65      70      75      80
309 Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro
310      85      90      95
312 Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn
313      100      105      110
315 Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu
316      115      120      125
318 Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr
319      130      135      140
321 Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala
322 145      150      155      160
324 Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu
325      165      170      175
327 Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala
328      180      185      190
330 Glu Val Glu Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu
331      195      200      205
333 Thr Ser Lys Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys
334      210      215      220
336 Ala Pro Val Glu Asn Thr Ala Glu Val Glu Thr Ser Lys Ala Leu Val
337 225      230      235      240

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VERIFICATION SUMMARY

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Input Set : A:\Uvm-0001.app

Output Set: N:\CRF3\11132000\I698579.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number